

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/525,020A
Source: IFW/6
Date Processed by STIC: 7-14-06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 07/14/2006

PATENT APPLICATION: US/10/525,020A

TIME: 09:30:49

Input Set : A:\81356233.APP

Output Set: N:\CRF4\07142006\J525020A.raw

3 <110> APPLICANT: YAMAMOTO, KAZUO
 4 SATO, AKIRA
 5 SHIMAUCHI, JUNKO
 6 MATSUMOTO, MARIKO
 8 <120> TITLE OF INVENTION: CARBOHYDRATE LIBRARY CONSTRUCTED BY GENE ALTERATION OF
 9 CARGO RECEPTORS
 11 <130> FILE REFERENCE: 081356-0233
 13 <140> CURRENT APPLICATION NUMBER: 10/525,020A
 14 <141> CURRENT FILING DATE: 2005-02-18
 16 <150> PRIOR APPLICATION NUMBER: PCT/JP03/01718
 17 <151> PRIOR FILING DATE: 2003-02-18
 19 <150> PRIOR APPLICATION NUMBER: JP 2002-238559
 20 <151> PRIOR FILING DATE: 2002-08-19
 22 <160> NUMBER OF SEQ ID NOS: 33
 24 <170> SOFTWARE: PatentIn Ver. 3.3
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 2768
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (22)..(1554)
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 38 1 5 10
 40 gcc aga gtt cgg ccg ctg ttc tgc gcc ttg ctg ctg tca ctc ggt cgc 99
 41 Ala Arg Val Arg Pro Leu Phe Cys Ala Leu Leu Leu Ser Leu Gly Arg
 42 15 20 25
 44 ttc gtc cgg ggc gac ggc gtg gga gga gac ccc gcg gtc gcg ttg cca 147
 45 Phe Val Arg Gly Asp Gly Val Gly Gly Asp Pro Ala Val Ala Leu Pro
 46 30 35 40
 48 cat cgc cgt ttc gag tac aaa tac agc ttc aag ggg ccg cac ctg gtg 195
 49 His Arg Arg Phe Glu Tyr Lys Tyr Ser Phe Lys Gly Pro His Leu Val
 50 45 50 55
 52 cag agc gac ggg acc gtg ccc ttc tgg gcc cac gcg ggg aat gct att 243
 53 Gln Ser Asp Gly Thr Val Pro Phe Trp Ala His Ala Gly Asn Ala Ile
 54 60 65 70
 56 cca agt tca gat caa att cga gta gca cca tct tta aaa agc caa aga 291
 57 Pro Ser Ser Asp Gln Ile Arg Val Ala Pro Ser Leu Lys Ser Gln Arg
 58 75 80 85 90
 60 ggc tca gtg tgg aca aag aca aaa gcg gcc ttt gag aac tgg gaa gtt 339
 61 Gly Ser Val Trp Thr Lys Thr Lys Ala Ala Phe Glu Asn Trp Glu Val

(pg.6)

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65	Glu	Val	Thr	Phe	Arg	Val	Thr	Gly
66				110				115
68	cta	gca	att	tgg	tat	gca	gaa	aat
69	Leu	Ala	Ile	Trp	Tyr	Ala	Glu	Asn
70				125				130
72	gga	tca	gct	gat	ctg	tgg	aat	ggt
73	Gly	Ser	Ala	Asp	Leu	Trp	Asn	Gly
74				140				145
76	gac	aat	gat	gga	aag	aaa	aat	aat
77	Asp	Asn	Asp	Gly	Lys	Lys	Asn	Asn
78	155							160
80	aat	gga	caa	atc	cat	tat	gac	cat
81	Asn	Gly	Gln	Ile	His	Tyr	Asp	His
82								175
84	ttg	gca	agt	tgc	cag	agg	gac	ttc
85	Leu	Ala	Ser	Cys	Gln	Arg	Asp	Phe
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88	gca	aag	att	acc	tat	tac	cag	aac
89	Ala	Lys	Ile	Thr	Tyr	Tyr	Gln	Asn
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93	Gly	Phe	Thr	Pro	Asp	Lys	Asn	Asp
94								220
96	aat	atg	att	atc	cct	gca	caa	ggg
97	Asn	Met	Ile	Ile	Pro	Ala	Gln	Gly
98	235							240
100	gga	ggt	ctt	gca	gat	gac	cat	gat
101	Gly	Gly	Leu	Ala	Asp	Asp	His	Asp
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104	ttg	act	gaa	cct	gga	aaa	gag	ccg
105	Leu	Thr	Glu	Pro	Gly	Lys	Glu	Pro
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108	gaa	aag	gaa	aaa	gaa	aag	tat	cag
109	Glu	Lys	Glu	Lys	Glu	Lys	Tyr	Gln
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116	caa	ggg	cag	cct	gcg	gag	gaa	ata
117	Gln	Gly	Gln	Pro	Ala	Glu	Glu	Ile
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121	Leu	Arg	Gln	Val	Phe	Glu	Gly	Gln
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126								350

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132 ggg cag cat ggg cag att act caa caa gaa ctg gat act gtt gtg aaa 1203
133 Gly Gln His Gly Gln Ile Thr Gln Gln Glu Leu Asp Thr Val Val Lys
134      380      385      390
136 act cag cat gag att ctg aga caa gta aat gaa atg aaa aat tcc atg 1251
137 Thr Gln His Glu Ile Leu Arg Gln Val Asn Glu Met Lys Asn Ser Met
138 395      400      405      410
140 agt gaa acc gtc aga ctg gtc agt gga atg cag cac cct ggc tct gct 1299
141 Ser Glu Thr Val Arg Leu Val Ser Gly Met Gln His Pro Gly Ser Ala
142      415      420      425
144 gga ggc gtc tat gag aca aca cag cac ttc att gac atc aaa gag cac 1347
145 Gly Gly Val Tyr Glu Thr Thr Gln His Phe Ile Asp Ile Lys Glu His
146      430      435      440
148 ctg cac ata gta aag agg gac ata gat aac tta gtg cag cga aat atg 1395
149 Leu His Ile Val Lys Arg Asp Ile Asp Asn Leu Val Gln Arg Asn Met
150      445      450      455
152 cca tca aat gaa aag ccg aaa tgc cca gaa cta cca cca ttt cca tca 1443
153 Pro Ser Asn Glu Lys Pro Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser
154      460      465      470
156 tgt ttg tct acg gtc cac ttc att ata ttt gtt gtg gtg caa act gta 1491
157 Cys Leu Ser Thr Val His Phe Ile Ile Phe Val Val Val Gln Thr Val
158 475      480      485      490
160 tta ttc att ggt tat atc atg tat agg tct cag caa gaa gca gct gcc 1539
161 Leu Phe Ile Gly Tyr Ile Met Tyr Arg Ser Gln Gln Glu Ala Ala Ala
162      495      500      505
164 aaa aaa ttc ttt tga ctaccatttt cctgtgtact tcattctatatt gtgtacaaaa 1594
165 Lys Lys Phe Phe
166      510
168 tgagtcgttt tgagggaatt taagtattta aattgcttca tagtctaaat tattaatttt 1654
170 ctttaataaaa taactgttta aacattgatt tgcagttaag aataaacctt aaagcaaaga 1714
172 caaccacatt ttaatttggt cacagtatgt aaatctgtct aaatttcagt gaatttctgg 1774
174 tcagtatgat gcagcctctg agcagaatat tgaccagtaa gagggtaaat aaagtggggg 1834
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178 gtaaacacac ttgccctcat gccctccaga atatgaggtc taattaagaa gtccatcagg 1954
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198 ttgcatactc ttttaaatca aggaggctgt agtagaggca gttttaagat tcttgaaggc 2554
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202 tgtgaagcac ttgttagtaa acttaacctt gaaatgtcag actggaagga gtttttatgt 2674
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210 <211> LENGTH: 510
211 <212> TYPE: PRT
212 <213> ORGANISM: Homo sapiens
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219           20           25           30
221 Val Gly Gly Asp Pro Ala Val Ala Leu Pro His Arg Arg Phe Glu Tyr
222           35           40           45
224 Lys Tyr Ser Phe Lys Gly Pro His Leu Val Gln Ser Asp Gly Thr Val
225           50           55           60
227 Pro Phe Trp Ala His Ala Gly Asn Ala Ile Pro Ser Ser Asp Gln Ile
228   65           70           75           80
230 Arg Val Ala Pro Ser Leu Lys Ser Gln Arg Gly Ser Val Trp Thr Lys
231           85           90           95
233 Thr Lys Ala Ala Phe Glu Asn Trp Glu Val Glu Val Thr Phe Arg Val
234           100          105          110
236 Thr Gly Arg Gly Arg Ile Gly Ala Asp Gly Leu Ala Ile Trp Tyr Ala
237           115          120          125
239 Glu Asn Gln Gly Leu Glu Gly Pro Val Phe Gly Ser Ala Asp Leu Trp
240           130          135          140
242 Asn Gly Val Gly Ile Phe Phe Asp Thr Phe Asp Asn Asp Gly Lys Lys
243 145           150           155           160
245 Asn Asn Pro Ala Ile Val Ile Ile Gly Asn Asn Gly Gln Ile His Tyr
246           165           170           175
248 Asp His Gln Asn Asp Gly Ala Ser Gln Ala Leu Ala Ser Cys Gln Arg
249           180           185           190
251 Asp Phe Arg Asn Lys Pro Tyr Pro Val Arg Ala Lys Ile Thr Tyr Tyr
252           195           200           205
254 Gln Asn Thr Leu Thr Val Met Ile Asn Asn Gly Phe Thr Pro Asp Lys
255           210           215           220
257 Asn Asp Tyr Glu Phe Cys Ala Lys Val Glu Asn Met Ile Ile Pro Ala
258 225           230           235           240
260 Gln Gly His Phe Gly Ile Ser Ala Ala Thr Gly Gly Leu Ala Asp Asp
261           245           250           255
263 His Asp Val Leu Ser Phe Leu Thr Phe Gln Leu Thr Glu Pro Gly Lys
264           260           265           270
266 Glu Pro Pro Thr Pro Asp Lys Glu Ile Ser Glu Lys Glu Lys Glu Lys
267           275           280           285
269 Tyr Gln Glu Glu Phe Glu His Phe Gln Gln Glu Leu Asp Lys Lys Lys
270           290           295           300
272 Glu Glu Phe Gln Lys Gly His Pro Asp Leu Gln Gly Gln Pro Ala Glu
273 305           310           315           320
275 Glu Ile Phe Glu Ser Val Gly Asp Arg Glu Leu Arg Gln Val Phe Glu
276           325           330           335
278 Gly Gln Asn Arg Ile His Leu Glu Ile Lys Gln Leu Asn Arg Gln Leu

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Output Set: N:\CRF4\07142006\J525020A.raw

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284 Glu Ile Ser Lys Arg Gly Ala Gly Met Pro Gly Gln His Gly Gln Ile
285          370          375          380
287 Thr Gln Gln Glu Leu Asp Thr Val Val Lys Thr Gln His Glu Ile Leu
288 385          390          395          400
290 Arg Gln Val Asn Glu Met Lys Asn Ser Met Ser Glu Thr Val Arg Leu
291          405          410          415
293 Val Ser Gly Met Gln His Pro Gly Ser Ala Gly Gly Val Tyr Glu Thr
294          420          425          430
296 Thr Gln His Phe Ile Asp Ile Lys Glu His Leu His Ile Val Lys Arg
297          435          440          445
299 Asp Ile Asp Asn Leu Val Gln Arg Asn Met Pro Ser Asn Glu Lys Pro
300          450          455          460
302 Lys Cys Pro Glu Leu Pro Pro Phe Pro Ser Cys Leu Ser Thr Val His
303 465          470          475          480
305 Phe Ile Ile Phe Val Val Val Gln Thr Val Leu Phe Ile Gly Tyr Ile
306          485          490          495
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314 <211> LENGTH: 1407
315 <212> TYPE: DNA
316 <213> ORGANISM: Homo sapiens
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320 <222> LOCATION: (1)..(1071)
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325 1 5 10 15
327 ctg gga agg cct ggg ctt ctc ggc ccc ggc cct ggc ccc act aca cct 96
328 Leu Gly Arg Pro Gly Leu Leu Gly Pro Gly Pro Gly Pro Thr Thr Pro
329 20 25 30
331 ctc ttt ctt ctt ttg ttg ttg ggg tct gtg act gcg gat ata act gac 144
332 Leu Phe Leu Leu Leu Leu Leu Gly Ser Val Thr Ala Asp Ile Thr Asp
333 35 40 45
335 ggc aac agt gaa cat ctc aag cgg gag cat tcg ctc att aag ccc tac 192
336 Gly Asn Ser Glu His Leu Lys Arg Glu His Ser Leu Ile Lys Pro Tyr
337 50 55 60
339 caa ggg gtc ggt tcc agc tct atg ccc ctc tgg gac ttc cag ggc agc 240
340 Gln Gly Val Gly Ser Ser Ser Met Pro Leu Trp Asp Phe Gln Gly Ser
341 65 70 75 80
343 act atg ctc acg agc cag tac gta cgt ctg acc cct gac gag cgc agc 288
344 Thr Met Leu Thr Ser Gln Tyr Val Arg Leu Thr Pro Asp Glu Arg Ser
345 85 90 95
347 aaa gag ggc tct atc tgg aac cac cag ccg tgc ttc ctc aaa gac tgg 336
348 Lys Glu Gly Ser Ile Trp Asn His Gln Pro Cys Phe Leu Lys Asp Trp

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/525,020A

DATE: 07/14/2006
TIME: 09:30:51

Input Set : A:\81356233.APP
Output Set: N:\CRF4\07142006\J525020A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; N Pos. 13, 14, 16, 17, 18, 20, 25, 26, 28, 29, 31, 32, 34, 35

Seq#:14; N Pos. 12, 13, 15, 16, 18, 19, 24, 25, 27, 28, 30, 31, 33, 34

VERIFICATION SUMMARY

DATE: 07/14/2006

PATENT APPLICATION: US/10/525,020A

TIME: 09:30:51

Input Set : A:\81356233.APP

Output Set: N:\CRF4\07142006\J525020A.raw

L:574 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

L:700 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0